

W/113561

#2



SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANTS: Adams, Thomas R. et al.
- (ii) TITLE OF INVENTION: Methods and Compositions for the Production of Stably Transformed, Fertile, Monocot Plants and Cells Thereof
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: P.O. BOX 4433
 - (C) CITY: Houston
 - (D) STATE: TX
 - (E) COUNTRY: USA
 - (F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patent In Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: unknown
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION: unknown
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Parker, David L.
 - (B) REGISTRATION NUMBER: 32,165
 - (C) REFERENCE/DOCKET NUMBER: DEKA:055/PAR
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 512-320-7200
 - (B) TELEFAX: 512-474-7577
 - (C) TELEX: NOT APPLICABLE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acid residues
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Thr	Val	Pro	Glu	Leu	Asn	Cys	Glu	Met	Pro	Pro	Ser	Asp
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGGATCCGT CGACATGGTA AGCTTAGCGG GCCCC

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCGTCGA CCATGGCGCT TCAAGCTTC

29

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCAGCTGGTA CCGCGAAGTT CGAAGGGCT

29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTAGACAACA AAGCAGCAAC CATGCCAGC ATGCAAGGCC TCATGCATC

49

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGGGATGCA TGAGGCCTTG CATGCTGGCC ATGGTTGCTG CTTTGTGTTGT

49

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acid residues
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ser Met Gln Gly Leu Met His Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acid residues
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Lys Cys Met Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGUGAAGUG AAGUGAAG

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1845 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
1 5 10 15

AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC ACC GGT
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
20 25 30

TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
35 40 45

GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80	240
GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95	288
ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110	336
TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125	384
GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140	432
ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160	480
TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175	528
GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190	576
TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val 195 200 205	624
CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220	672
GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC GTG Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240	720
CTC GAT ATC GTG GCT CTG TTC CCA AAT TAC GAT AGC CGC CGC TAC CCA Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro 245 250 255	768
ATT CGA ACC GTG TCC CAA CTG ACC CGC GAA ATT TAC ACC AAC CCA GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270	816
CTG GAA AAT TTT GAT GGT AGC TTT CGC GGC TCC GCT CAG GGC ATC GAA Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285	864
CGC AGC ATT AGG AGC CCA CAT CTG ATG GAT ATC CTG AAC AGC ATC ACC Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300	912
ATC TAC ACC GAT GCT CAT AGG GGT TAC TAC TAC TGG TCC GGC CAT CAA Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln 305 310 315 320	960

ATC ATG GCT TCC CCT GTG GGC TTT TCC GGG CCA GAA TTC ACC TTT CCA Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335	1008
CTG TAC GGC ACG ATG GGC AAT GCC GCT CCA CAA CGC ATT GTG GCT Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 340 345 350	1056
CAA CTG GGT CAG GGC GTG TAC CGC ACC CTG TCC TCC ACC CTG TAC CGC Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 355 360 365	1104
CGC CCT TTT AAT ATC GGC ATC AAC AAC CAG CAA CTG TCC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 370 375 380	1152
GGC ACC GAA TTT GCT TAC GGC ACC TCC TCC AAT CTG CCA TCC GCT GTA Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 385 390 395 400	1200
TAC CGC AAG AGC GGC ACC GTG GAT TCC CTG GAT GAA ATC CCA CCA CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 405 410 415	1248
AAT AAC AAC GTG CCA CCT AGG CAA GGC TTT AGC CAT CGC CTG AGC CAT Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 420 425 430	1296
G TG TCC ATG TTT CGC TCC GGC TTT AGC AAT AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Val Ser Ile Ile 435 440 445	1344
CGC GCT CCT ATG TTC TCC TGG ATC CAT CGC AGC GCT GAA TTT AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 450 455 460	1392
ATC ATT GCC TCC GAT AGC ATT ACC CAA ATC CCT GCC GTG AAG GGC AAC Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn 465 470 475 480	1440
TTT CTG TTT AAT GGT TCC GTG ATT TCC GGC CCA GGC TTT ACC GGT GGC Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly 485 490 495	1488
GAC CTG GTG CGC CTG AAT AGC AGC GGC AAT AAC ATT CAG AAT CGC GGC Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly 500 505 510	1536
TAC ATT GAA GTG CCA ATT CAC TTC CCA ACC TCC ACC CGC TAC CGC Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg 515 520 525	1584
GTG CGC GTG CGC TAC GCT TCC GTG ACC CCA ATT CAC CTC AAC GTT AAC Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn 530 535 540	1632
TGG GGC AAT TCC TCC ATT TTT TCC AAT ACC GTG CCA GCT ACC GCT ACC Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr 545 550 555 560	1680
TCC CTG GAT AAT CTG CAA TCC AGC GAT TTT GGT TAC TTT GAA AGC GCC Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala 565 570 575	1728

AAT GCT TTT ACC TCC TCC CTG GGT AAT ATC GTG GGT GTG CGC AAT TTT Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe 580 585 590	1776
AGC GGC ACC GCC GGC GTG ATC ATC GAC CGC TTT GAA TTT ATT CCA GTG Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val 595 600 605	1824
ACC GCC ACC CTC GAG TAGGTA Thr Ala Thr Leu Glu 610	1845

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 613 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140
Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175
Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val 195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
465 470 475 480

Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
485 490 495

Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly
500 505 510

Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
515 520 525

Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
530 535 540

Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
 545 550 555 560

Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
 565 570 575

Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
 580 585 590

Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
 595 600 605

Thr Ala Thr Leu Glu
 610

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1848 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1 5 10 15	
AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
20 25 30	
TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
35 40 45	
GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
50 55 60	
TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
65 70 75 80	
GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC	288
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
85 90 95	
ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA	336
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu	
100 105 110	
TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA	384
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu	
115 120 125	

GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140	432
ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160	480
TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175	528
GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190	576
TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val 195 200 205	624
CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220	672
GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC ACC GTG Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240	720
CTC GAT ATC GTG GCT CTG TTC CCA AAT TAC GAT AGC CGC CGC TAC CCA Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro 245 250 255	768
ATT CGA ACC GTG TCC CAA CTG ACC CGC GAA ATT TAC ACC AAC CCA GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270	816
CTG GAA AAT TTT GAT GGT AGC TTT CGC GGC TCC GCT CAG GGC ATC GAA Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285	864
CGC AGC ATT AGG AGC CCA CAT CTG ATG GAT ATC CTG AAC AGC ATC ACC Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300	912
ATC TAC ACC GAT GCT CAT AGG GGT TAC TAC TAC TGG TCC GGC CAT CAA Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln 305 310 315 320	960
ATC ATG GCT TCC CCT GTG GGC TTT TCC GGG CCA GAA TTC ACC TTT CCA Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335	1008
CTG TAC GGC ACG ATG GGC AAT GCC GCT CCA CAA CAA CGC ATT GTG GCT Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 340 345 350	1056
CAA CTG GGT CAG GGC GTG TAC CGC ACC CTG TCC TCC ACC CTG TAC CGC Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 355 360 365	1104
CGC CCT TTT AAT ATC GGC ATC AAC AAC CAG CAA CTG TCC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 370 375 380	1152

GGC ACC GAA TTT GCT TAC GGC ACC TCC TCC AAT CTG CCA TCC GCT GTA Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 385 390 395 400	1200
TAC CGC AAG AGC GGC ACC GTG GAT TCC CTG GAT GAA ATC CCA CCA CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 405 410 415	1248
AAT AAC AAC GTG CCA CCT AGG CAA GGC TTT AGC CAT CGC CTG AGC CAT Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 420 425 430	1296
GTG TCC ATG TTT CGC TCC GGC TTT AGC AAT AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Val Ser Ile Ile 435 440 445	1344
CGC GCT CCT ATG TTC TCC TGG ATC CAC CGC TCC GCT GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 450 455 460	1392
ATC ATC CCG TCC TCC CAA ATC ACC CAA ATC CCG CTC ACC AAG TCC ACG Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 465 470 475 480	1440
AAC CTC GGC TCC GGC ACG TCC GTC GTC AAG GGC CCG GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 485 490 495	1488
GGC GAC ATC CTC CGC CGC ACG TCC CCG GGC CAG ATC TCC ACC CTC CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 500 505 510	1536
GTC AAC ATC ACG GCT CCG CTG AGC CAG CGC TAC AGG GTG CGC ATC AGA Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 515 520 525	1584
TAC GCT AGC ACG ACC AAC CTG CAA TTC CAC ACG TCC ATC GAC GGC AGA Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 530 535 540	1632
CCG ATC AAC CAG GGC AAC TTC AGC GCG ACG ATG AGC TCC GGG TCC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 545 550 555 560	1680
CTC CAG TCC GGC TCC TTC CGC ACG GTC GGT TTC ACC ACG CCG TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 565 570 575	1728
TTC TCC AAC GGC TCC TCC GTC TTC ACG CTC TCC GCT CAC GTC TTC AAC Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 580 585 590	1776
TCC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTC CCG GCC GAG Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 595 600 605	1824
GTC ACC TTC GAG CTC GAG TAGGTA Val Thr Phe Glu Leu Glu 610	1848

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
595 600 605

Val Thr Phe Glu Leu Glu
610

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANTS: ADAMS, THOMAS R. et al.
10 (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TRANSFORMED, FERTILE MONOCOT
PLANTS AND CELLS THEREOF

15 (iii) NUMBER OF SEQUENCES: 13
10 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: ARNOLD, WHITE & DURKEE
(B) STREET: P.O. BOX 4433
(C) CITY: HOUSTON
(D) STATE: TEXAS
20 (E) COUNTRY: USA
(F) ZIP: 77210

25 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1

30 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: UNKNOWN
(B) FILING DATE: TO BE INSERTED
(C) CLASSIFICATION: UNKNOWN

35 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: PARKER, DAVID L.
(B) REGISTRATION NUMBER: 32,165
(C) REFERENCE/DOCKET NUMBER: DEKA:055/PAR

40 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 512-320-7200
(B) TELEFAX: 512-474-7577
(C) TELEX: NOT APPLICABLE

(2) INFORMATION FOR SEQ ID NO:1:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acid residues
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Thr Val Pro Glu Leu Asn Cys Glu Met Pro Pro Ser Asp
1 5 10 15

10 (3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGGATCCGT CGACATGGTA AGCTTAGCGG GCCCC

35

25 (4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCGTCGA CCATGGCGCT TCAAGCTTC

29

40 (5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCAGCTGGTA CCGCGAAGTT CGAAGGGCT

29

5 (6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15 CTAGACAACA AAGCAGCAAC CATGGCCAGC ATGCAAGGCC TCATGCATC 49

20 (7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

30 CCGGGATGCA TGAGGCCTTG CATGCTGGCC ATGGTTGCTG CTTTGTG 49

35 (8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 11 amino acid residues
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

45 Met Ala Ser Met Gln Gly Leu Met His Pro Gly
1 5 10

50 (9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acid residues
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Lys Cys Met Gln Val
10 1 5

(10) INFORMATION FOR SEQ ID NO:9:

15

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

25 AAGUGAAGUG AAGUGAAG

18